In the Specification:

Please delete the paragraph on page 3, lines 3-6, and replace it with the following paragraph:

In WO 99/15004 a chimeric construct for modifying the composition of storage organs in plants is described. A gene encoding a sulphur-rich protein is provided with a C-terminal KDEL **(SEQ ID NO: 18)** extension, which enables targeting of the construct to the endoplasmic reticulum and Golgi apparatus.

Please delete the paragraph on page 7, lines 1-9, and replace it with the following paragraph:

Figure 3 shows the nucleotide sequence of a histidine codon-enriched sequence (A), the nucleotide sequence **(SEQ ID NO: 19)** of a cysteine-methionine codon enriched sequence **(SEQ ID NO: 20)** (B), the nucleotide sequence **(SEQ ID NO: 21)** of a glycine codon-enriched sequence **(SEQ ID NO: 22)** (C) and the nucleotide sequence **(SEQ ID NO: 23)** of a lysine codon-enriched sequence **(SEQ ID NO: 24)** (D). The protein translation sequence **(SEQ ID NO: 26)** is shown below the nucleotide sequence **(SEQ ID NO: 25)**. K, lysine; H, histidine; R, arginine; V, valine; G, glycine; L, leucine; C, cystine; S, serine; M, methionine. The asterisk indicates the transcriptional termination codon. Restriction sites used in cloning are shown in bold and are indicated above the sequence.

Please delete the paragraph on page 33, line 9 to page 10, line 7 and replace it with the following paragraph:

Most of the oleosin N-terminal sequence region is hydrophobic, whereas the amino acid sequence of the oleosin C-terminal portion encoded by the second exon of the oleosin gene represents hydrophilic sequence that is suitable for expression in *E. coli* and using as the antigen in immunizations. Therefore, the C-terminal oleosin region (aa 120-173) was selected for this purpose. The second exon of the oleosin gene was amplified in a PCR reaction using the plasmid pOLE4/11 (Example 6) as the template and the oligonucleotide primers:

OLE-EX-B (SEQ ID NO:15) (5'-TGTGGGATCCTACGCAACGGGAGAGCACCCA) and

OLE-3'XhoI (SEQ ID NO:12) (5'-GCGCCTCGAGAAGTAGTGTGCTGGCCACCAC)

containing *Bam*HI restriction site and *Xho*I restriction site, respectively. The resulting PCR product was digested with *Bam*HI and *Xho*I and cloned into *Xho*I- and *Bam*HI-digested pGEM-7Zf(+) (Promega Corporation, USA; catalogue number P2251). After restriction analysis of the resulting clones and sequencing, clone pGEM-OLE2EX was selected for the subsequent cloning steps. To obtain an expression construct, the region of the oleosin second exon was removed from pGEM-OLE2EX by digestion with *Bam*HI and *Xho*I and cloned into the (*Bam*HI and *Sal*I digested) expression vector pQE30 (QIAGEN). In the resulting construct pQE-OLE2EX, the 3'-

terminal portion of the oleosin gene was translationally fused to a leader sequence containing a 6xHis tag **(SEQ ID NO: 27)**, which makes it possible to affinity purify the expressed product. The plasmid pQE-OLE2EX was transformed into *E. coli* strain M15 [pREP4] (QIAGEN). Induction of recombinant protein expression was carried out in Luria broth by adding IPTG to a final concentration 1 mM followed by incubation on a rotary shaker at 220 rpm for 2-4 h at 37°C. The *E. coli* cells were collected from induced and non-induced control cultures, and expression of the recombinant protein was analyzed by SDS-PAGE. For SDS-PAGE, 12.5% acrylamide gels were prepared. Gels were run at 100V/500mA for 45 1 h, and subsequently stained in CBB (0.05% Coomassie Brilliant Blue, 50% methanol, 7% glacial acetic acid) and destained in 7% methanol/5% acetic acid. In the induced cultures, a major band was evident that was absent in the non-induced cultures. Mobility of this band corresponded to the expected mobility of the His-tagged C-terminal portion of the oleosin gene (8.3 kDa).